CLAIMS

1. An isolated nucleic acid molecule consisting of SEQ ID NO 1, its complementary form and the RNA form thereof.

2. An isolated nucleic acid molecule consisting of SEQ ID NO 2, its complementary form and the RNA form thereof.

3. An isolated nucleic acid molecule that specifically hybridizes to SEQ ID NO 1 or 2, or to the RNA form of said SEQ ID NO 1 or 2 wherein T is replaced by U, or to the complementary form of said SEQ ID NO 1or 2, or to a fragment of at least 20 contiguous nucleotides thereof, or to any of their homologues, for the detection and/or identification of *Enterococcus* species, in particular of *E. faecalis* and/or *E. faecium*.

4. An isolated nucleic acid molecule according to claim 3 consisting of a nucleic acid selected from the group consisting of SEQ ID NO 22 to 26, 28 to 43, 45 to 65 and 67 to 84.

5. A set of two or three polynucleotide probes, said probes hybridizing specifically to SEQ ID NO 1 or SEQ ID NO 2 or homologues, or to their RNA form wherein T is replaced by U, or to their complementary form, wherein there are no more than 25 nucleotides between said probes.

6. A set of two or three polynucleotide probes according to claim 5 consisting of any combinations of Table 3.

7. A composition comprising at least one nucleic acid molecule according to any of claims 1 to 4 and/or a set of two polynucleotide probes according to claim 5 or claim 6.

8. Use of a nucleic acid molecule consisting of SEQ ID NO 1 or 2, or of the RNA form of said SEQ ID NO 1 or 2 wherein T is replaced by U, or of the complementary form of said SEQ ID NO 1or 2, or of a fragment of at least 20

contiguous nucleotides thereof, or of any of their homologues, for the detection and/or identification of *Enterococcus* species, in particular of *E. faecalis* and/or *E. faecium*.

9. A method for detecting or identifying *Enterococcus* species using at least one nucleic acid molecule according to any of claims 1 to 4.

10. A method according to claim 9 for detection and/or identification of *Enterococcus* species in a sample comprising the steps of:

(i) if need be releasing, isolating and/or concentrating the polynucleic acids in the sample;

(ii) if need be amplifying the 16S-23S rRNA spacer region, or a fragment comprising the target sequence, or the target sequence or a fragment thereof, with at least one suitable primer pair;

(iii) hybridizing the polynucleic acids of step (i) or (ii) with at least one polynucleotide probe that hybridizes to the target sequence,
wherein the target sequence of step (ii) and (iii) consists of SEQ ID NO 1 or 2 or homologues thereof, or to their RNA form wherein T is replaced by U, or to their complementary form, or a to a fragment of at least 20 contiguous nucleotides thereof,

(iv) detecting the hybrids formed, and

(v) interpreting the signal(s) obtained and inferring the presence of *Enterococcus* species and/or identifying the *Enterococcus* species in the sample.

11. A method according to claim 10 wherein a suitable primer pair consists any combination of a forward primer polynucleotide selected from the group consisting of SEQ ID NO 3, 4, 5, 6, 7, 8, 9, 10 or 11 and their homologues, and a reverse primer polynucleotide selected from the group consisting of SEQ ID NO 12, 13, 14, 15, 16, 17, 18, 19, 20 or 21 and their homologues.

12. A method according to claim 10 or claim 11 wherein two polynucleotide probes are used.

13. A method according to claim 12 wherein the two polynucleotide probes hybridize to the target sequence adjacent to each other with less than 25 nucleotides in between.

14. A method according to claim 12 or 13 wherein the two polynucleotide probes consist of any combination of polynucleotides of Table 3.

15. A kit for detection and/or identification of *Enterococcus* species comprising the following components:

- at least one nucleic acid molecule according to any of claims 1 to 4 and/or a set of two polynucleotide probes according to claim 5 or 6.
- a hybridization buffer, or components necessary for producing said buffer.